Figure 1

Stability Study of SAHH
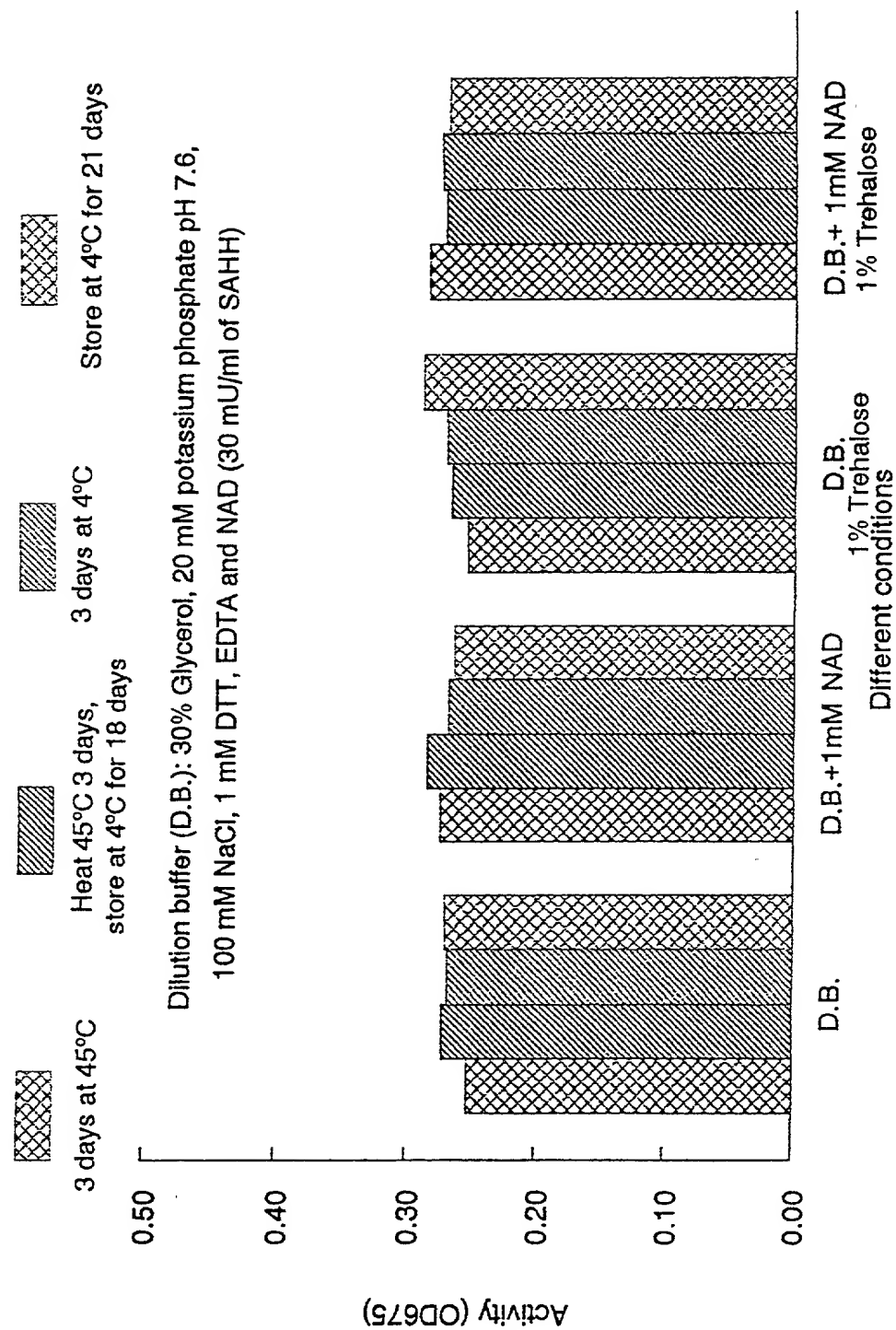
3 days at 45°C

Heat 45°C 3 days,
store at 4°C for 18 days

3 days at 4°C

Store at 4°C for 21 days

Dilution buffer (D.B.): 30% Glycerol, 20 mM potassium phosphate pH 7.6,
100 mM NaCl, 1 mM DTT, EDTA and NAD (30 mU/ml of SAHH)

Activity (OD675)

0.50
0.40
0.30
0.20
0.10
0.00

D.B.

D.B.+1mM NAD

D.B.
1% Trehalose

D.B.+ 1mM NAD
1% Trehalose

Different conditions

Figure 2

Figure 3

Nco I

pTrc

His·SAHH

BamH I

5 S

rrnBT1T2

pTrcHis·SAHH

Amp^r

lac P^r

PRO₂₅₀₇

L
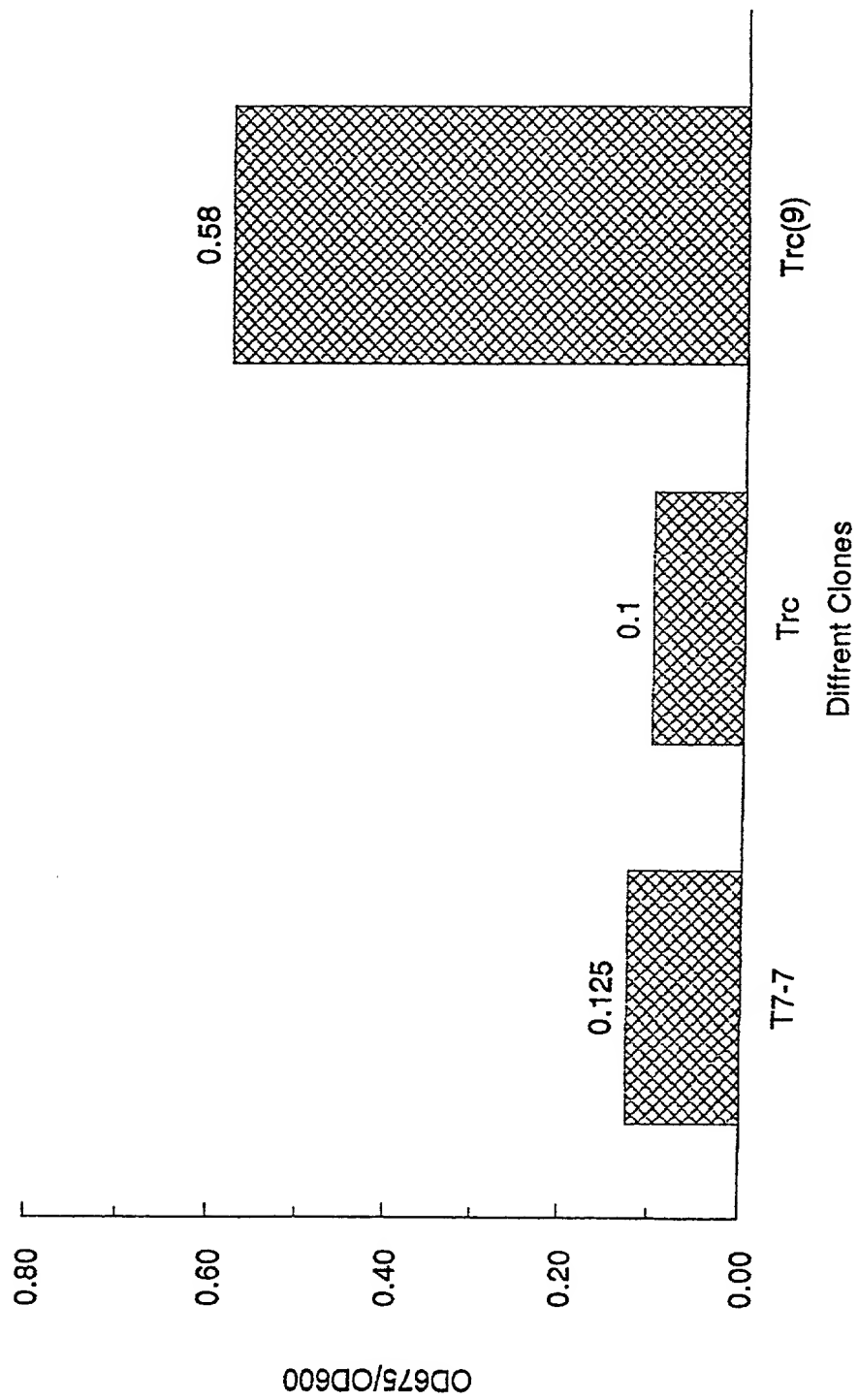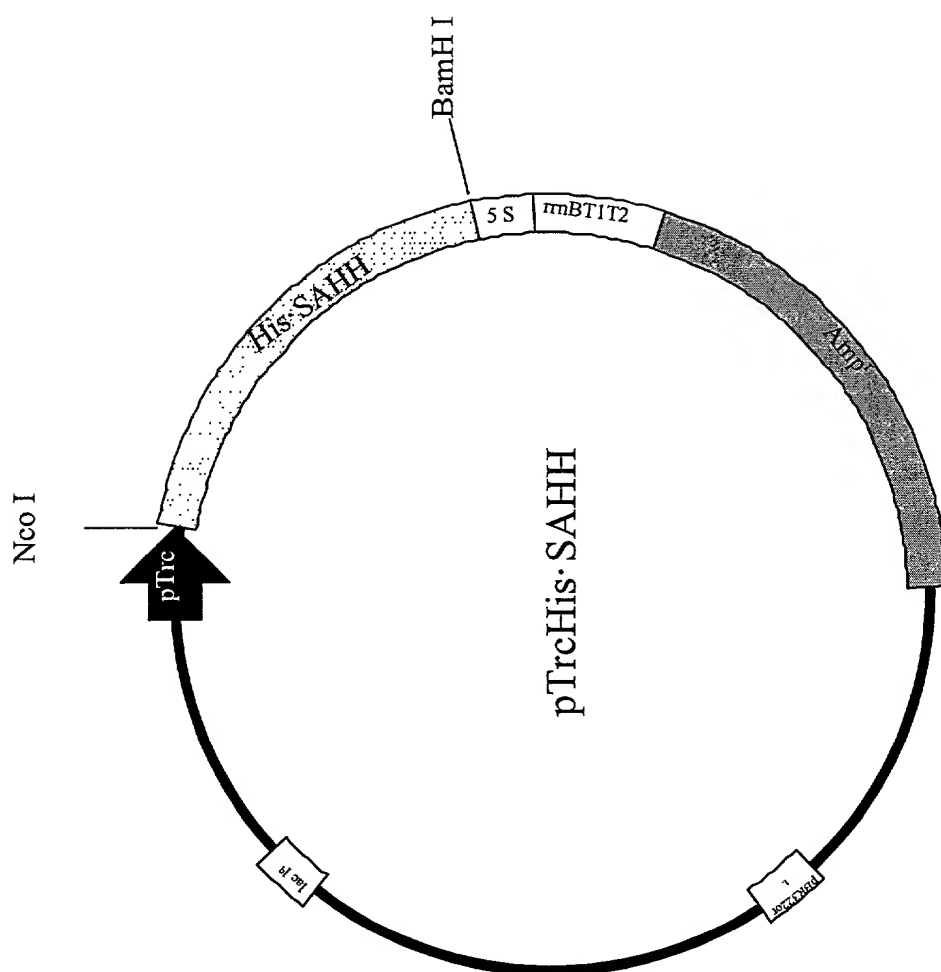
Figure 4

Stability of SAHH.His

3 days incubation in different temperature

Figure 5
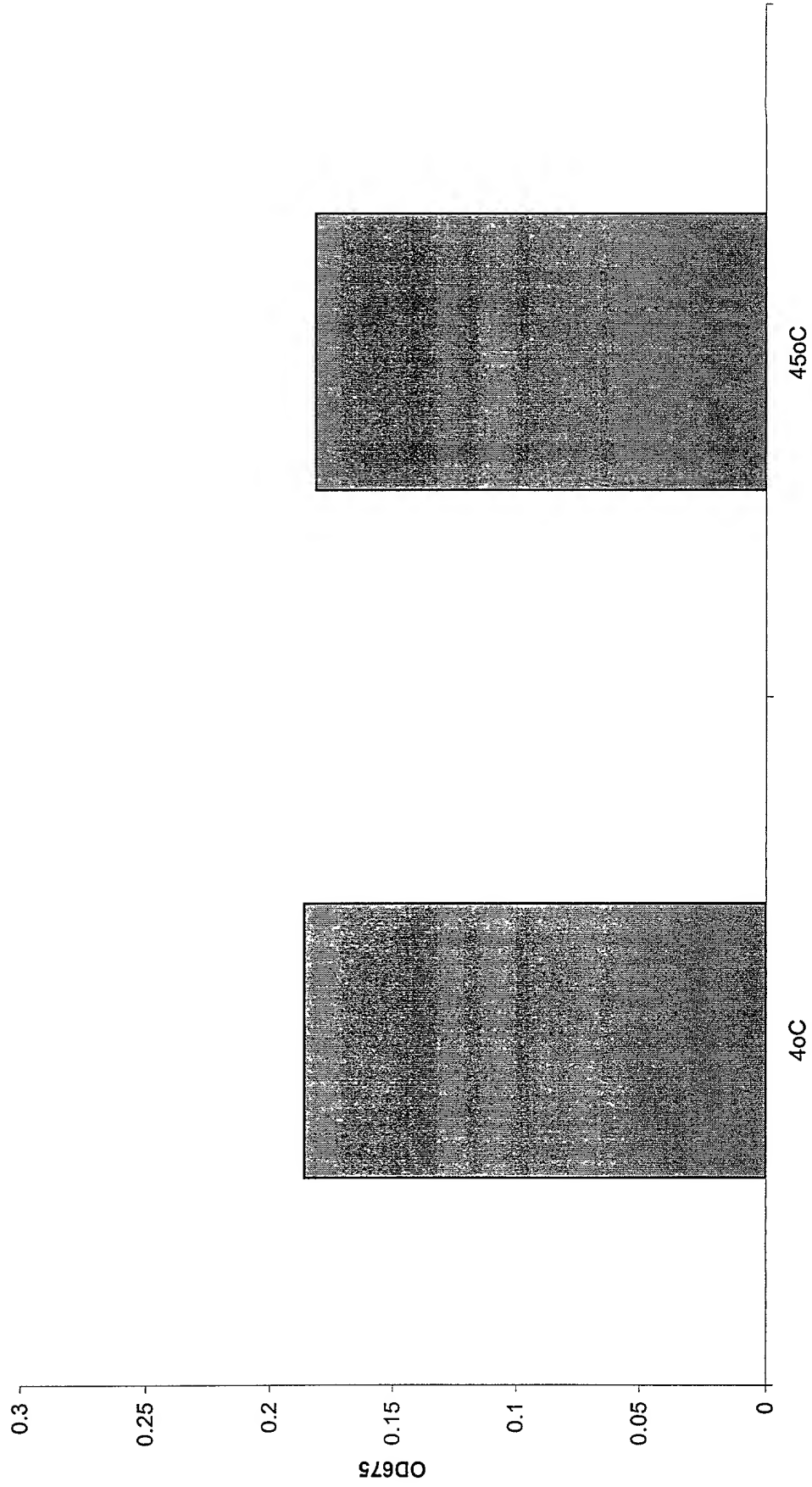
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SIM - Results of the Alignment

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: Wild (1882 residues)
Sequence 2: A/C, (1594 residues)

using the parameters:

Number of alignments computed: 20
Cost of a matching aligned pair: 1
Cost of a transition: -1
Cost of a transversion: -1
Gap open penalty: 6.0
Gap extension penalty: 0.2

[handwritten annotations:] Accession GenBank. U 40872 TVU-40872. and gi|1183??? T vaginalis deposited 10/31/?6 Baguara, A S ... Mol Biochem Parasit (1996) 81 (-11)

Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH. **new**.

```
99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

Wild    291 ATGGCTTGCAAATCACCTGCTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC
A/C,     71 ATGGCTTGCAAATCACCTACTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC   SEQ ID NO.1
            ****************** *****************************************

Wild    351 CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,    131 CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
            ***********************************************************

Wild    411 CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC
```

Figure 6a

```
A/C,          191 CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC
                  ****************************** *****************************

Wild          471 CACATGACAGTCCAGACAGCGGTCCTTATTGAGACACTCACAGCTCTTGGTGCTGATGTC
A/C,          251 CACATGACAGTCCAGACAGCCGTCCTCATCGAGACACTCACAGCTCTTGGTGCTGATGTC
                  ******************** *****  ** *****************************

Wild          531 AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
A/C,          311 AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
                  ***********************************************************

Wild          591 GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
A/C,          371 GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
                  ***********************************************************

Wild          651 ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
A/C,          431 ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
                  ***********************************************************

Wild          711 CCACAGCAGGTTGTCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,          491 CCACAGCAGGTTGTCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
                  ***********************************************************

Wild          771 TTCGAAACAGCCGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
A/C,          551 TTCGAAACAGCCGGTGCTGTTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
                  ******************** **************************************

Wild          831 GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
A/C,          611 GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
                  ***********************************************************

Wild          891 GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
A/C,          671 GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
                  ***********************************************************

Wild          951 GAGAAGGAGGGCAAACTCCTCTTCCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,          731 GAGAAGGAGGGCAAACTCCTCTTCCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
                  ***********************************************************

Wild         1011 AAGTTCGATAACATCTACGGCTGTCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
A/C,          791 AAGTTCGATAACATCTACGGCTGCCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
                  ***********************  **********************************

Wild         1071 GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC
A/C,          851 GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGCAAGGGC
                  **************************************************** ******

Wild         1131 TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCTATC
A/C,          911 TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCAATC
                  ******************************************************* ***

Wild         1191 TGCGCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
A/C,          971 TGCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
                  **************** ******************************************

Wild         1251 GATGTCGATATCTTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
A/C,         1031 GATGTCGATATCTTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
                  ***********************************************************

Wild         1311 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
A/C,         1091 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
                  ***********************************************************

Wild         1371 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
```

Figure 6b

```
A/C,        1151 ACAGATGGCC1CATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
                 --- -- -**************************************************

Wild        1431 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
A/C,        1211 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
                 ***********************************************************--

Wild        1491 CTTGGTTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTCACAAACCAGACA
A/C,        1271 CTTGGCTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTCACAAACCAGACA
                 ***** *****************************************************

Wild        1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTTACACACTT
A/C,        1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTTACACACTT
                 *******************************************  ***************

Wild        1611 CCGAAGCATCTCGATGAAGAAGTCGTTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
A/C,        1391 CCGAAGCATCTCGATGAAGAAGTCGCTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
                 *************************  *********************************

Wild        1671 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
A/C,        1451 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
                 ***********************************************************

Wild        1731 TCTGATGCTTACCGTTATTAA
A/C,        1511 TCTGATGCTTACCGTTATTAA
                 ********************
```

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

```
Wild         782 CGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACC
A/C,         682 CGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACC
                 *****  *   *  **** *****  ** **  *  ***  *   ****
```

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild        1053 GGTATCAACCGTGCTTCCGA
A/C,         674 GGCATGAACGGTGTTTCCGA
                 ** ** *** *** ******
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild         564 GATACAGCCGCTGCTG
A/C,         554 GAAACAGCCGGTGCTG
                 ** ******* *****
```

64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild        1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC
A/C,         710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACTCCTC
                 **** **** ** *   *   *** ***** * *   ** **
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild         774 GAAACAGCCGGTGCTG
A/C,         344 GATACAGCCGCTGCTG
                 ** ******* *****
```

Figure 6c

12-27 1999 4:22 PM